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TCG CAC AGC CTT GCC TTG CTC CTC TGC TCC TCC GTC GTC AGC TCC GTC	60
Ser His Ser Leu Ala Leu Leu Cys Ser Val Leu Ser Ser Val	115
Met Gly Ala Pro Arg Ile	
1 5	
TAC GCA CTG GTG GAT GCC GAT GTC ATA ACG AAG GAG CAG CAG ATC	163
Tyr Ala Leu Val Asp Ala Asp Asp Val Ile Thr Lys Glu Glu Gln Ile	211
25 30 35	
ATT CTT CTG CGC AAT GCC CAG GCC CAG TGT GAG CAG CGC CTG AAA GAG	259
Ile Leu Leu Arg Asn Ala Gln Ala Gln Cys Glu Gln Arg Leu Lys Glu	
40 45 50	
GTC CTC AGG GTC CCT GAA CTT GCT GAA TCT GCC AAA GAC TGG ATG TCA	307
Val Leu Arg Val Pro Glu Leu Ala Glu Ser Ala Lys Asp Trp Met Ser	
55 60 65 70	
AGG TCT GCA AAG ACA AAG AAG GAG AAA CCT GCA GAA AAG CTT TAT CCC	355
Arg Ser Ala Lys Thr Lys Lys Glu Lys Pro Ala Glu Lys Leu Tyr Pro	
75 80 85	
CAG GCA GAG GAG TCC AGG GAA GTT TCT GAC AGG AGC CGG CTG CAG GAT	403
Gln Ala Glu Glu Ser Arg Glu Val Ser Asp Arg Ser Arg Leu Gln Asp	
90 95 100	
GGC TTC TGC CTA CCT GAG TGG GAC AAC ATT GTG TGG CCT GCT GGA	451
Gly Phe Cys Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Ala Gly	
105 110 115	

FIG. 1A

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GTG CCC GGC AAG GTG GTG GCC GTC CCC TGC CCC GAC TAC TAC GAC	499
Val Pro Gly Lys Val Val Ala Val Pro Cys Pro Asp Tyr Phe Tyr Asp	
120 125	
TTC AAC CAC AAA GGC CGA GCC TAT CGG CGC TGT GAC AGC AAT GGC AGC	547
Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser	
135 140 145	150
TGG GAG CTG GTG CCT GGG AAC AAC CGG ACA TGG GCG AAT TAC AGC GAA	595
Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu	
155	160
TGT GTC AAG TTT CTG ACC AAC GAG ACC CGG GAA CGG GAA GTC TTT GAT	643
Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp	
170	175
CGC CTC GGA ATG ATC TAC ACT GTG GGC TAC TCC ATC TCT CTG GGC TCC	691
Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser	
185	190
195	
CTC ACT GTG GCT GTG CTG ATT CTG GGT TAC TTT AGG AGG TTA CAT TGC	739
Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys	
200	205
210	
ACC CGA AAC TAC ATT CAC ATG CAT CTC TTC GTG TCC TTT ATG CTC CGG	787
Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg	
215	220
225	
GCT GTA AGC ATC TTC ATC AAG GAT GCT GTG CTC TAC TCG GGG GTT TCC	835
Ala Val Ser Ile Phe Ile Lys Asp Ala Val Leu Tyr Ser Gly Val Ser	
235	240
245	

FIG. 1B

ACA	GAT	GAA	ATC	GAG	CGC	ATC	ACC	GAG	GAG	CTG	AGG	GCC	TTC	ACA	883	
Thr	Asp	Glu	Ile	Glu	Arg	Ile	Thr	Glu	Glu	Glu	Leu	Arg	Ala	Phe	Thr	
															250	
															255	
GAG	CCT	CCC	CCT	GCT	GAC	AAG	GCG	GCT	TTT	GTG	GGC	TGC	GTG	GCG	931	
Glu	Pro	Pro	Pro	Ala	Asp	Lys	Ala	Gly	Phe	Val	Gly	Cys	Arg	Val	Ala	
															265	
															270	
GTA	ACC	GTC	TTC	CTT	TAC	TTC	CTG	ACC	AAC	TAC	TAC	TGG	ATC	CTG	979	
Val	Thr	Val	Phe	Leu	Tyr	Phe	Leu	Thr	Thr	Asn	Tyr	Tyr	Trp	Ile	Leu	
															280	
															285	
GTG	GAA	GGC	CTC	TAC	CTT	CAC	AGC	CTC	ATC	TTC	ATG	GCT	TTT	TTC	TCT	1027
Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser	
															305	
															300	
GAG	AAA	AAG	TAT	CTC	TGG	GGT	TTC	ACA	TTA	TTT	GGC	TGG	GGC	CTC	CCT	1075
Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Leu	Phe	Gly	Trp	Gly	Leu	Pro	
															315	
															320	
GCC	GTG	TTT	GTC	GCT	GTG	TGG	GTG	ACC	GTG	AGG	GCT	ACA	CTG	GCC	AAC	1123
Ala	Val	Phe	Val	Ala	Val	Trp	Val	Thr	Val	Arg	Ala	Thr	Leu	Ala	Asn	
															330	
															335	
ACT	GAG	TGC	TGG	GAC	CTG	AGT	TCG	GGG	AAT	AAG	AAA	TGG	ATC	ATA	CAG	1171
Thr	Glu	Cys	Trp	Asp	Leu	Ser	Ser	Gly	Asn	Lys	Lys	Trp	Ile	Ile	Gln	
															345	
															350	
GTG	CCC	ATC	CTG	GCA	GCT	ATT	GTG	GTG	AAC	TTT	ATT	CTT	TTT	ATC	AAT	1219
Val	Pro	Ile	Leu	Ala	Ala	Ile	Val	Val	Asn	Phe	Ile	Leu	Phe	Ile	Asn	
															365	
															370	

FIG. 1C

ATA	ATC	AGA	GTC	CTG	GCT	ACT	AAA	CTC	CGG	GAG	ACC	AAT	GCA	GGG	AGA	1267	
Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Leu	Arg	Thr	Asn	Ala	Gly	Arg	375
																380	
TGT	GAC	AGC	AGG	CAA	CAG	TAT	AGA	AAG	CTG	CTG	AAG	TCC	ACG	CTA	GTC	1315	
Cys	Asp	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Lys	Ser	Thr	Leu	Val		395
																400	
CTC	ATG	CCG	CTA	TTT	GGG	GTG	CAC	TAC	ATC	GTC	TTC	ATG	GCC	ACG	CCG	1363	
Leu	Met	Pro	Leu	Phe	Gly	Val	His	Tyr	Ile	Val	Phe	Met	Ala	Thr	Pro		410
																415	
TAC	ACA	GAA	GTA	TCA	GGG	ATT	CTT	TGG	CAA	GTC	CAA	ATG	CAC	TAT	GAA	1411	
Tyr	Thr	Glu	Val	Ser	Gly	Ile	Leu	Trp	Gln	Val	Gln	Met	His	Tyr	Glu		425
																420	
ATG	CTC	TTC	AAT	TCA	TTC	CAG	GGG	TTT	TTC	GTT	GCC	ATT	ATA	TAC	TGT	1459	
Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys		440
																445	
TTC	TGC	AAT	GGA	GAG	GTA	CAA	GCA	GAG	ATC	AAG	TCA	TGG	AGC	CGA	1507		
Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Ser	Trp	Ser	Arg		455	
																460	
TGG	ACC	CTG	GCC	TTG	GAC	TTC	AAG	CGG	AAG	GCC	CGG	AGT	GGC	AGC	AGT	1555	
Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser		475
																480	
ACC	TAC	AGC	TAT	GGC	CCC	ATG	GTG	TCA	CAT	ACA	AGT	GTC	ACC	AAT	GTG	1603	
Thr	Tyr	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn		490
																495	
																500	

FIG. 1D

GGA	CCT	CGA	GGG	GGC	TGG	CCT	TGT	CCC	TCA	GCC	CTC	GAC	TAGCTCCCTGG	1652	
Gly	Pro	Arg	Gly	Gly	Trp	Pro	Cys	Pro	Ser	Ala	Leu	Asp			
505													510		
														515	
GGCTGGAGCC	AGTGCCAATG	GCCATCACCA	GTTCCTGGC	TATGTGAAGC	ATGGTTCCAT	1712									
TCTGAGAAC	TCATTGCCTT	CATCTGGCCC	AGAGCCTGGC	ACCAAAGATG	ACGGGTATCT	1772									
CAATGGCTCT	GGACTTTATG	AGCCAATGGT	TGGGAAACAG	CCCCCTCCAC	TCCTGGAGGA	1832									
GGAGAGAG	ACAGTCATGT	GACCCATATC				1862									

FIG. 1E

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TGGCACAGC	CACCCCTGTG	GTA	GTC	CCGG	GGCCAGCCCCA	CTGAGCTGGC	ATATCAGCTG	60								
GTGCCCGT	TGGACTCGGC	CCTAGGGAAC	GGGGGG	ATG	GGA	CCC	CGG	ATC	115							
Ser	His	Leu	Ala	Leu	Leu	Cys	Ser	Val	Leu	Pro	Arg	Ile	5			
													1			
TAC	GCA	CTG	GTG	GCC	TTG	CTC	TGC	TGC	TCC	GTG	CTC	AGC	TCC	GTG	163	
Tyr	Ala	Leu	Val	Asp	Ala	Asp	Val	Ile	Thr	Lys	Glu	CAG	GAG	CAG	ATC	211
															35	
ATT	CTT	CTG	CGC	AAT	GCC	CAG	GCC	CAG	TGT	GAG	CAG	CGC	CTG	AAA	GAG	259
Ile	Leu	Leu	Arg	Asn	Ala	Gln	Ala	Gln	Cys	Glu	Gln	Arg	Leu	Lys	Glu	40
															50	
GTC	CTC	AGG	GTC	CCT	GAA	CCT	GCT	GAA	TCT	GCC	AAA	GAC	TGG	ATG	TCA	307
Val	Leu	Arg	Val	Arg	Pro	Glu	Leu	Ala	Glu	Ser	Ala	Lys	Asp	Trp	Met	70
															65	
AGG	TCT	GCA	AAG	ACA	AAG	AAG	GAG	AAA	CCT	GCA	GAA	AAG	CCT	TAT	CCC	355
Arg	Ser	Ala	Lys	Thr	Lys	Lys	Glu	Lys	Pro	Ala	Glu	Lys	Leu	Tyr	Pro	85
CAG	GCA	GAG	TCC	AGG	GAA	GTT	TCT	GAC	AGG	AGC	CGG	CTG	CAG	GAT	403	
Gln	Ala	Glu	Glu	Ser	Arg	Glu	Val	Ser	Asp	Arg	Ser	Arg	Leu	Gln	Asp	100
															95	
GGC	TTC	TGC	CTA	CCT	GAG	TGG	GAC	AAC	ATT	GTG	TGG	CCT	GCT	GGA	451	
Gly	Phe	Cys	Leu	Pro	Glu	Trp	Asp	Asn	Ile	Val	Cys	Trp	Pro	Ala	Gly	115
															110	
GTC	CCC	GCC	AAG	GTC	GTC	GCC	GTC	CCC	TCC	CCC	GAC	TAC	TTC	TAC	GAC	499
Val	Pro	Gly	Lys	Val	Val	Ala	Val	Pro	Cys	Pro	Asp	Tyr	Phe	Tyr	Asp	120
															125	

FIG. 2A

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TTC AAC CAC AAA GGC CGA GCC TAT CGG CGC TGT GAC AGC AAT GGC AGC	547
Phe Asn His Lys Gly Arg Ala Tyr Arg Arg Cys Asp Ser Asn Gly Ser	
135 140 145 150	
TGG GAG CTG GTG CCT GGG AAC AAC CGG ACA TGG GCG AAT TAC AGC GAA	595
Trp Glu Leu Val Pro Gly Asn Asn Arg Thr Trp Ala Asn Tyr Ser Glu	
155 160 165	
TGT GTC AAG TTT CTG ACC AAC GAG ACC CGG GAA CGG GAA GTC TTT GAT	643
Cys Val Lys Phe Leu Thr Asn Glu Thr Arg Glu Arg Glu Val Phe Asp	
170 175 180	
CGC CTC GGA ATG ATC TAC ACT GTG GGC TAC TCC ATC TCT CTG GGC TCC	691
Arg Leu Gly Met Ile Tyr Thr Val Gly Tyr Ser Ile Ser Leu Gly Ser	
185 190 195	
CTC ACT GTG GCT GTG CTG ATT CTG GGT TAC TTT AGG AGG TTA CAT TGC	739
Leu Thr Val Ala Val Leu Ile Leu Gly Tyr Phe Arg Arg Leu His Cys	
200 205 210	
ACC CGA AAC TAC ATT CAC ATG CAT CTC RTC GTG TCC TTT ATG CTC CGG	787
Thr Arg Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg	
215 220 225 230	
GCT GTA AGC ATC TTC ATC AAG GAT GCT GTG CTC TAC TCG GGG GTT TCC	835
Ala Val Ser Ile Phe Ile Lys Asp Ala Val Leu Tyr Ser Gly Val Ser	
235 240 245	

FIG. 2B

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ACA GAT GAA ATC GAG CGC ATC ACC GAG GAG CTG AGG GCC TTC ACA	883
Thr Asp Glu Ile Glu Arg Ile Thr Glu Glu Leu Arg Ala Phe Thr	
250 255 260	
 GAG CCT CCC GCT GAC AAG GCG GGT TTT GTG GGC TGC AGA GTG GCG	931
Glu Pro Pro Ala Asp Lys Ala Gly Phe Val Gly Cys Arg Val Ala	
265 270 275	
 GTA ACC GTC TTC CTT TAC TTC CTG ACC AAC TAC TAC TGG ATC CTG	979
Val Thr Val Phe Leu Tyr Phe Leu Thr Asn Tyr Trp Ile Leu	
280 285 290	
 GTG GAA GGC CTC TAC CTT CAC AGC CTC ATC TTC ATG GCT TTT TCT	1027
Val Glu Gly Leu Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser	
295 300 305	
 GAG AAA AAG TAT CTC TGG GGT TTC ACA TTA TTT GGC TGG CCC CTC CCT	1075
Glu Lys Tyr Leu Trp Gly Phe Thr Leu Phe Gly Trp Gly Leu Pro	
315 320 325	
 GCC GTG TTT GTC GCT GTG TGG GTG ACC GTG AGG GCT ACA CTG GCC AAC	11123
Ala Val Phe Val Ala Val Trp Val Thr Val Arg Ala Thr Leu Ala Asn	
330 335 340	
 ACT GAG TGC TGG GAC CTG AGT TCG GGG AAT AAG AAA TGG ATC ATA CAG	11171
Thr Glu Cys Trp Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln	
345 350 355	
 GTG CCC ATC CTG GCA GCT ATT GTG GTG AAC TTT ATT CTT TTT ATC AAT	1219
Val Pro Ile Leu Ala Ala Ile Val Val Phe Ile Leu Phe Ile Asn	
360 365 370	
 ATA ATC AGA GTC CTG GCT ACT AAA CTC CGG GAG ACC AAT GCA GGG AGA	1267
Ile Ile Arg Val Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg	
375 380 385	
390	

FIG. 2C

TGT	GAC	ACG	AGG	CAA	CAG	TAT	AGA	AAG	CTG	CTG	AAG	TCC	ACG	CTA	GTC	1315
Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Lys	Ser	Thr	Leu	Val	
				395				400								405
CTC	ATG	CCG	CTA	TTT	GGG	GTG	CAC	TAC	ATC	GTC	TTC	ATG	GCC	ACG	CCG	1363
Leu	Met	Pro	Leu	Phe	Gly	Val	His	Tyr	Ile	Val	Phe	Met	Ala	Thr	Pro	
			410				415									420
TAC	ACA	GAA	GTA	TCA	GGG	ATT	CTT	TGG	CAA	GTC	CAA	ATG	CAC	TAT	GAA	1411
Tyr	Thr	Glu	Val	Ser	Gly	Ile	Leu	Trp	Gln	Val	Gln	Met	His	Tyr	Glu	
			425				430									435
ATG	CTC	TTC	AAT	TCA	TTC	CAG	GGA	TTT	TTC	GTC	ATT	ATA	TAC	TGT	TGT	1459
Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Val	Ala	Ile	Ile	Tyr	Cys	
			440				445									450
TTC	TGC	AAT	GGA	GAG	GTA	CAA	GCA	GAG	ATC	AAG	AAG	TCA	TGG	AGC	CGA	1507
Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Lys	Ser	Trp	Ser	Arg	
			455				460									470
TGG	ACC	CTG	GCC	TTG	GAC	TTC	AAG	CGG	AAG	GCC	CGG	AGT	GGC	AGC	AGT	1555
Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	
			475				480									485
ACC	TAC	AGC	TAT	GGC	CCC	ATG	GTG	TCA	CAT	ACA	AGT	GTC	ACC	AAT	GTG	1603
Thr	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	
			490				495									500

FIG. 2D

GGA CCT CGA GGG GGG CTC GCC TGT TCC CTC AGC CCT CGA CTA GCT CCT
Gly Pro Arg Gly Gly Leu Ala Leu Ser Pro Arg Leu Ala Pro
505 510 515

GGG GCT GGA GCC AGT GCC AAT GGC CAT CAC CAG TTG CCT GGC TAT GTG
Gly Ala Gly Ala Ser Ala Asn Gly His His Gln Leu Pro Gly Tyr Val
520 525 530 535

AAG CAT GGT TCC ATT TCT GAG AAC TCA TTG CCT TCA TCT GGC CCA GAG
Lys His Gly Ser Ile Ser Glu Asn Ser Leu Pro Ser Ser Gly Pro Glu
535 540 545 550

CCT GGC ACC AAA GAT GAC GGG TAT CTC AAT GGC TCT GGA CTT TAT GAG
Pro Gly Thr Lys Asp Asp Gly Tyr Leu Asn Gly Ser Gly Leu Tyr Glu
555 560 565 570

CCA ATG GTT GGG GAA CAG CCC CCT CCA CTC CTG GAG GAG AGA GAG
Pro Met Val Gly Glu Gln Pro Pro Pro Leu Leu Glu Glu Arg Glu
570 575 580

ACA GTC ATG TGACCCATAT C
Thr Val Met
585 590 595 600

FIG. 2E

GGGGGGGG	GGGGGGGA	GCTGGAGGC	GGGGGGGC	TGCCCCGAGG	GACGGGGCCC	60
TAGGGGTGG	CG ATG GGG GCC CGC CCC ATC GCA CCC AGC CTG GCG CTC					
Met Gly Ala Ala Arg Ile Ala Pro Ser Leu Ala Leu						
1	5	10	15	20	25	
CTA CTC TGC TGC CCA GTRG CTC AGC TCC GCA TAT GCG CTG GTG GAT GCG						
Leu Leu Cys Cys Pro Val Leu Ser Ser Ala Tyr Ala Leu Val Asp Ala						
15	20	25				
GAC GAT GTC TTT ACC AAA GAG GAA CAG ATT TTC CTG CTG CAC CGT GCC						
Asp Asp Val Phe Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala						
30	35	40				
CAG GCG CAA TGT GAC AAG CTG CTC AAG GAA GTT CTG CAC ACA GCA GCC						
Gln Ala Gln Cys Asp Lys Leu Leu Lys Glu Val Ile Phe Leu Thr Ala Ala						
45	50	55	60			
AAC ATA ATG GAG TCA GAC AAG GGC TGG ACA CCA GCA TCT ACG TCA GGG						
Asn Ile Met Glu Ser Asp Lys Gly Trp Thr Pro Ala Ser Thr Ser Gly						
65	70	75				
AAG CCC AGG AAA GAG AAG GCA TCG GGA AAG TTC TAC CCT GAG TCT AAA						
Lys Pro Arg Lys Glu Lys Ala Ser Gly Lys Phe Tyr Pro Glu Ser Lys						
80	85	90				
GAG AAC AAG GAC GTG CCC ACC GGC AGC AGG CGC AGA GGG CGT CCC TGT						
Glu Asn Lys Asp Val Pro Thr Gly Ser Arg Arg Arg Gly Arg Pro Cys						
95	100	105				
CTG CCC GAG TGG GAC AAC ATC GTT TGC TGG CCA TTA GGG GCA CCA GGT						
Leu Pro Glu Trp Asp Asn Ile Val Cys Trp Pro Leu Gly Ala Pro Gly						
110	115	120				
GAA GTG GTG GCA GTA CCT TGT CCC GAT TAC ATT TAT GAC TTC AAT CAC						
Glu Val Val Ala Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His						
125	130	135	140			

FIG. 3A

AAA	GGC	CAT	GCC	TAC	AGA	CGC	TGT	GAC	CGC	AAT	GGC	AGC	TGG	GAG	GTG	540
Lys	Gly	His	Ala	Tyr	Arg	Arg	Cys	Asp	Arg	Asn	Gly	Ser	Trp	Glu	Val	
145																155
GTT	CCA	GGG	CAC	AAC	CGG	ACG	TGG	GCC	AAC	TAC	AGC	GAG	TGC	CTC	AAG	588
Val	Pro	Gly	His	Asn	Arg	Thr	Trp	Ala	Asn	Tyr	Ser	Glu	Cys	Leu	Lys	
160																170
TTC	ATG	ACC	AAT	GAG	ACG	CGG	GAA	CGG	GAG	GTA	TTT	GAC	CGC	CTA	GGC	636
Phe	Met	Thr	Asn	Glu	Thr	Arg	Glu	Arg	Glu	Val	Phe	Asp	Arg	Leu	Gly	
175																185
ATG	ATC	TAC	ACC	GTG	GGA	TAC	TCC	ATG	TCT	CTC	GCC	TCC	CTC	ACG	GTG	684
Met	Ile	Tyr	Thr	Val	Gly	Tyr	Ser	Met	Ser	Leu	Ala	Ser	Leu	Thr	Val	
190																200
GCT	GTC	CTC	ATC	CTG	GCC	TAT	TTT	AGG	CGG	CTG	CAC	TGC	ACG	CGC	AAC	732
Ala	Val	Ile	Leu	Ala	Tyr	Phe	Arg	Arg	Leu	Arg	Leu	His	Cys	Thr	Arg	
205																210
TAC	ATC	CAC	ATG	TTC	CTG	TCG	TTT	ATG	CTG	CGC	GCC	GCG	AGC		780	
Tyr	Ile	His	Met	His	Met	Phe	Leu	Ser	Phe	Met	Leu	Arg	Ala	Ala	Ser	
																225
ATC	TTC	GTG	AAG	GAC	GCT	GTG	CTC	TAC	TCT	GGC	TRC	ACG	CTG	GAT	GAG	828
Ile	Phe	Val	Lys	Asp	Ala	Val	Leu	Tyr	Ser	Gly	Phe	Thr	Leu	Asp	Glu	
240																245
																250

FIG. 3B

GCC	GAG	CGC	CTC	ACA	GAG	GAA	TTG	CAC	ATC	GCG	CAG	GTG	CCA	876			
Ala	Glu	Arg	Leu	Thr	Glu	Glu	Glu	Leu	His	Ile	Ile	Ala	Gln	Val	Pro		
255														265			
CCT	CCG	GGC	GCT	GCC	GCC	GTA	GGC	TAC	GCT	GGC	TGC	CGC	GCG	924			
Pro	Pro	Pro	Ala	Ala	Ala	Ala	Phe	Leu	Ala	Val	Gly	Tyr	Ala	Cys	Arg	Val	Ala
270														280			
GTG	ACC	TTC	TTC	CTC	TAC	TTC	CTG	GCT	ACC	AAC	TAC	TAC	TGG	ATT	CTG	972	
Val	Thr	Phe	Phe	Leu	Tyr	Phe	Leu	Ala	Thr	Asn	Tyr	Tyr	Tyr	Trp	Ile	Leu	
285														295	300		
GTG	GAG	GGG	CTG	TAC	TTG	CAC	CTC	ATC	TTC	ATG	GCC	TTT	TTC	TCA	1020		
Val	Glu	Gly	Leu	Tyr	Leu	His	Ser	Leu	Ile	Phe	Met	Ala	Phe	Phe	Ser		
305														310			
GAG	AAG	AAG	TAC	CTG	TTG	GGC	TTC	ACC	ATC	TTT	GGC	TGG	GGT	CTA	CCG	1068	
Glu	Lys	Lys	Tyr	Leu	Trp	Gly	Phe	Thr	Ile	Phe	Gly	Trp	Gly	Leu	Pro		
320														325			
GCT	GTC	TTC	GTG	GCT	GTG	TGG	GTC	AGA	GCA	ACC	TTC	GCC	AAC	1116			
Ala	Val	Phe	Val	Ala	Val	Trp	Val	Gly	Val	Arg	Ala	Thr	Leu	Ala	Asn		
335														340			
ACT	GGG	TGC	TGG	GAT	CTG	AGC	TCC	GGG	CAC	AAG	AAG	TGG	ATC	ATC	CAG	1164	
Thr	Gly	Cys	Trp	Asp	Leu	Ser	Ser	Gly	His	Lys	Lys	Trp	Ile	Ile	Gln		
350														355			
GTG	CCC	ATC	CTG	GCA	TCT	GTT	GTG	CTC	AAC	TTC	ATC	CTT	TTT	ATC	AAC	1212	
Val	Pro	Ile	Leu	Ala	Ser	Val	Val	Leu	Asn	Phe	Ile	Leu	Phe	Ile	Asn		
365														370			
ATC	ATC	CGG	GTG	CTT	GCC	ACT	AAG	CTT	CGG	GAG	ACC	AAT	GCG	GGC	CGG	1260	
Ile	Ile	Arg	Val	Leu	Ala	Thr	Lys	Leu	Arg	Glu	Thr	Asn	Ala	Gly	Arg		
385														390			
														395			

FIG. 3C

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TGT	GAC	ACC	AGG	CAG	CAG	TAC	CGG	AAG	CTG	CTC	AGG	TCC	ACG	TTG	GTG	1308
Cys	Asp	Thr	Arg	Gln	Gln	Tyr	Arg	Lys	Leu	Leu	Arg	Ser	Thr	Leu	Val	
			400					405								410
CTC	GTG	CCG	CTC	TTT	GGT	GTC	CAC	TAC	ACC	GTC	TTC	ATG	GCC	TTG	CCG	1356
Leu	Val	Pro	Leu	Phe	Gly	Val	His	Tyr	Thr	Val	Met	Ala	Leu	Pro		
			415					420								425
TAC	ACC	GAG	GTC	TCA	GGG	ACA	TG	TGG	CAG	ATC	CAG	ATG	CAT	TAT	GAG	1404
Tyr	Thr	Glu	Val	Ser	Gly	Thr	Leu	Trp	Gln	Ile	Gln	Met	His	Tyr	Glu	
			430						435							440
ATG	CTC	TTC	AAC	TCC	TTC	CAG	GGA	TTT	TTT	GTC	ATC	ATA	TAC	TGT	1452	
Met	Leu	Phe	Asn	Ser	Phe	Gln	Gly	Phe	Phe	Vai	Ala	Ile	Tyr	CYS		
			445				450			455						460
TTC	TGC	AAT	GGT	GAG	GTG	CAG	GCA	GAG	ATT	AGG	AAG	TCA	TGG	AGC	CGC	1500
Phe	Cys	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Arg	Lys	Ser	Trp	Ser	Arg	
			465						470							475
TGG	ACA	CTG	GCG	TTG	GAC	TTC	AAG	CGC	AAA	GCA	CGA	AGT	GGG	AGT	AGC	1548
Trp	Thr	Leu	Ala	Leu	Asp	Phe	Lys	Arg	Lys	Ala	Arg	Ser	Gly	Ser	Ser	
			480						485							490
AGC	TAC	AGC	TAT	GGC	CCA	ATG	GTG	TCT	CAC	ACG	AGT	GTG	ACC	AAT	GTG	1596
Ser	Tyr	Ser	Tyr	Gly	Pro	Met	Val	Ser	His	Thr	Ser	Val	Thr	Asn	Val	
			495						500							505

FIG. 3D

Gly	CCC	CGT	GCA	GGA	CTC	AGC	CTC	CCC	CTG	CGC	CTG	CCT	1644	
Pro	Pro	Arg	Ala	Gly	Leu	Ser	Leu	Pro	Leu	Pro	Arg	Leu	Pro	Pro
510					515					520				
Gly	GCC	ACT	ACC	AAT	GGC	CAC	TCC	CAG	CTG	CCT	GGC	CAT	GGC	1692
Ala	Ala	Thr	Thr	Asn	Gly	His	Ser	Gln	Leu	Pro	Gly	His	Ala	Lys
525					530					535			Pro	Gly
GCT	CCA	GCC	GCT	GAG	ACT	GAA	ACC	CTA	CCA	GTC	ACT	ATG	GCG	1740
Ala	Ala	Pro	Ala	Thr	Glu	Thr	Glu	Thr	Leu	Pro	Val	Thr	Met	Vall
					545					550			Pro	
AAG	GAC	GAT	GGA	TTC	CTT	AAC	GGC	TCC	TGC	TCA	GCA	CTG	GTT	CCC
Lys	Asp	Asp	Gly	Phe	Leu	Asn	Gly	Ser	Cys	Ser	Gly	Leu	Asp	Glu
					560				565				570	
GCC	TCC	GGG	TCT	GCG	CGG	CCT	CCA	TTG	TTG	CAG	GAA	TGG	GAG	1788
Ala	Ser	Gly	Ser	Ala	Arg	Pro	Pro	Pro	Leu	Leu	Gln	Glu	Gly	Trp
					575					580			Glu	
ACA	GTC	ATG	TGACTGGCA	CTAGGGCT	AGACTGCTGG	CCTGGGCCACA								1885
Thr	Val	Met												
TGGACAGATG	GACCAAGAAG	CCAGTGTGTG	GCTGGTTGGAT	TATTGGGGAT	CTGGACCCAGG	1945								
AAGATAACAA	AAGGAAATG	GAAGTGGACG	AAGCAGAGAA	GAAGGAAGAG	GTTTGGCAGG	2005								
AATTAAATAT	GTTTCCCTCAG	TGGGATGATG	AGGACACAAAG	GAAGGCC		2051								

FIG. 3E

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1 MGAARIAPSLALLCCPVLSAYALVDADDVFTKEEQIFLLHRAQAQCDK 50
1 MGAPRISHSLALLCCSVLSSVYALVDADDVITKEEQIILLRNAQAQCEQ 50

51 LLKEVLHTAANIMESDKGWT PASTSGKPRKEASGKFYPESKENKDVTG 100
51 RLKEVLR.VPELAESAKDW..MSRSAKTKKEKPAAEKLYPQAEESREVSDR 97

101 SRRGRPCLPEWDNIVCWPLGAPGEVVAVPCPDYIYDFNHKGAYRRCDR 150
98 SRLQDGFCCLPEWDNIVCWPAVGPGKVAVPCPDYFYDFNHKGGRAYRRCD 147

151 NGSWEVPGHNRWTWANYSECLKFMTNETREREVFDRLGMIYTVGYSMSLA 200
148 NGSWELVPGNNRTWANYSECVKFLTNETREREVFDRLGMIYTVGYSISLG 197

201 SLTVAVLILAYFRLHCTRNYIHMHMFLSFMLRAASIFVKDAVLYSGFTL 250
198 SLTVAVLILGYFRLHCTRNYIHMHLFVFSMLRAVSIFIKDAVLYSGVST 247

251 DEAERLTEEELHIIAQVPPPPAAAAGVYAGCRVAVTFFLYFLATNYYWIL 300
248 DEIERITEEELRAFTE...PPPADKAGFVGCRVAVTVFLYFLTTNYYWIL 294

301 VEGLYLHSIFMAFFSEKKYLWGFTIFGWGLPAVFVAWWGV RATLANTG 350
295 VEGLYLHSIFMAFFSEKKYLWGFTLFGWGLPAVFVAWWVTVRATLANTE 344

351 CWDLSSGHKKWIIQVPILASVVLNFILFINIIRVLATKLRETNAGRC DTR 400
345 CWDLSSGNKKWIIQVPILAAIVVN FILFINIIRVLATKLRETNAGRC DTR 394

401 QQYRKLLRSTLVLVPLFGVHYTVFMALPYTEVSGTLWQIQMHYEMLFNSF 450
395 QQYRKLLKSTLVLMPPLFGVHYIVFMATPYTEVSGILWQVQMHYEMLFNSF 444

451 QGFFVAIICYFCNGEVQAEIRKWSRWTLALDFKRKARSGSSSYGPMV 500
445 QGFFVAIICYFCNGEVQAEIKKWSRWTLALDFKRKARSGSSTSYGPMV 494

501 SHTSVTNGPRAGLSLPLSPRLPP...ATTNGHSQLPCHAKPGAPATE 547
495 SHTSVTNGPRGLALSLSPRLAPGAGASANGMHQLPGYVKGSISEN 544

548 TLPVTMAVPKDDGFLNGSCSGLDEEASGSARPPPLLQEGWETVM 591
545 PSSGPEPGTKDDGYLNG..SGLYEPMVG.EQPPPILLEERETVM 585

Gap Weight: 3.000 Average Match: 0.540
Length Weight: 0.100 Average Mismatch: -0.396

Quality: 712.2 Length: 594
Ratio: 1.215 Gaps: 6
Percent Similarity: 87.113 Percent Identity: 77.835

FIG. 4

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R15 MGAARIAPSL ALLLCCPVLS SAYALVDADD VFTKEEQIFL LHRAQAQCDK 50
 Oko MGAPRISHSL ALLLCCSVLS SVYALVDADD VITKEEQIIL LRNAQAQCEQ 50
 Okh MGAPRISHSL ALLLCCSVLS SVYALVDADD VITKEEQIIL LRNAQAQCEQ 50
 ----- A -----

R15 LLKEVLTAA NIMESDKGWT PASTSGKPRK EKASGKFYPE SKENKDVPCTC 100
 Oko RLKEVLR.VP ELAESAKDW. .MSRSAKTKK EKPAEKLYPQ AEEREVSDR 97
 Okh RLKEVLR.VP ELAESAKDW. .MSRSAKTKK EKPAEKLYPQ AEEREVSDR 97

* * * * *
 R15 SRRRGPCPLP EWDNIVCWPL GAPGEVVAVP CPDYIYDFNH KGHAYRRCDR 150
 Oko SRLQDGFCPLP EWDNIVCWPA GVPGKVVAVP CPDYFYDFNH KGRAYRRCDS 147
 Okh SRLQDGFCPLP EWDNIVCWPA GVPGKVVAVP CPDYFYDFNH KGRAYRRCDS 147
 ----- B -----

N N * N
 R15 NGSWEVVPGH NRTWANYSEC LKFLTNETRE REVFDRLGMI YTVGYSMSLA 200
 Oko NGSWELVPGN NRTWANYSEC VKFLTNETRE REVFDRLGMI YTVGYSISLG 197
 Okh NGSWELVPGN NRTWANYSEC VKFLTNETRE REVFDRLGMI YTVGYSISLG 197

R15 SLTVAVLILA YFRLHLCTR N YIHMHMFLSF MLRAASIFVK DAVLYSGFTL 250
 Oko SLTVAVLILG YFRLHLCTR N HIHMHLFVSF MLRAVSIFIK DAVLYSGVST 247
 Okh SLTVAVLILG YFRLHLCTR N YIHMHMFLSF MLRAVSIFIK DAVLYSGVST 247
 -- C ----- D -----

* * * * *
 R15 DEAERLTEEE LHIIAQVPPP PAAAAGYAG CRVAVTFFLY FLATNYYWIL 300
 Oko DEIERITEEE LRAFTE...P PPADKAGFVG CRVAVTVFLY FLTTNYYWIL 294
 Okh DEIERITEEE LRAFLT...P PPADKAGFVG CRVAVTVFLY FLTTNYYWIL 294
 ----- E -----

R15 VEGLYLHSLI FMAFFSEKKY LWGFTLFGWG LPAPVFVAVVV GVRATLANTG 350
 Oko VEGLYLHSLI FMAFFSEKKY LWGFTLFGWG LPAPVFVAVVV TVRATLANTE 344
 Okh VEGLYLHSLI FMAFFSEKKY LWGFTLFGWG LPAPVFVAVVV TVRATLANTE 344
 ----- F ----- G -----

* * * * *
 R15 CWDLSSGHKK WIIQVPILAS VVNLNFIILFIN IIRVLATKLR ETNAGRCCTR 400
 Oko CWDLSSGNKK WIIQVPILAA IVVNFIILFIN IIRVLATKLR ETNAGRCCTR 394
 Okh CWDLSSGNKK WIIQVPILAA IVVNFIILFIN IIRVLATKLR ETNAGRCCTR 394
 ----- H -----

R15 QOYRKLLRST LVLVPLFGVH YTVMALPYT EVSGTGWQIQ MHYEMLFNSF 450
 Oko QOYRKLLKST LVLMPLFGVH YIVFMATPYT EVSGILWQVQ MHYEMLFNSF 444
 Okh QOYRKLLKST LVLMPLFGVH YIVFMATPYT EVSGILWQVQ MHYEMLFNSF 444
 ----- I -----

R15 QGFFVAIICY FCNGEVQAEI RKSWSRWTLA LDFKRKARSG SSSSYGPMV 500
 Oko QGFFVAIICY FCNGEVQAEI KKWSWSRWTLA LDFKRKARSG SSTSYGPMV 494
 Okh QGFFVAIICY FCNGEVQAEI KKWSWSRWTLA LDFKRKARSG SSTSYGPMV 494
 -- J -----

R15 SHTSVTNVGP RAGLSLPLSP RLPP...ATT NGHSQLPGHA KPGAPATETE 547
 Oko SHTSVTNVGP RGGLALSLSP RLAPGAGASA NGHHQLPGYV KHGSISENSL 544
 Okh SHTSVTNVGP RGG..... .WPCPSA LD 515

R15 TLPVTMAVPK DDGFLNGSCS GLDEEASGSA RPPPLLQEGW ETVM 591
 Oko PSSGPEPGTK DDGYLNG..S GLYEPMVG.E QPPPLLEER ETVM 585

With I enzymes: SACI

GGGATCCGGCCCTAGGCCGTGGCAtgggACCCGCCggatcgccaccggcctggcg
2 ----- 61
CCCTAGGGGCCGGATCCGCCACCGCTacccCTggCGGgcctagcgtggccggaccgc
62 -----
M G T A R I A P G L A -

ctcctgctctgctgcccgtqctcagctccgcgtacgcqctggatgcagatgacgtc
121 -----
gaggacgagacgacggggcacgagtcgaggcgcatgcgcgaccacctacgtctactcag
L L C C P V L S S A Y A L V D A D D V -

atgactaaagaggaacagatcttcctgtgcacccgtgctcaggcccagtgcaaaaacgg
122 ----- 181
tactgatttctcc'tt'gtctagaaggacccatcagtgccggtcacgcttttgc
M T K E E Q I F L L H R A Q A Q C E K R -

ctcaaggaggctgtcagaggccagccagcataatggaaatcagacaaggatggacatct
182 ----- 241
gagttccctccaggacgtctccgggtcggtcgtagtaccattaccttagtctgttccctacactgtaga
L K E V L Q R P A S I M E S D K G W T S -

gcgtccacatcaggaaaggccaggaaagataaggcatctggaaaggctctaccctgagatct
242 ----- 301
cgcagggttagtcccttaggtccctatccgttagacccttcgagatggactcaga
A S T S G K P R K D K A S G K L Y P E S -

FIG. 6A

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302 gaggaggacaaggcaccacccactggcaggaaaccgaggcgccccctgtctgccggaa

ctccctcttccgtgggtgaccctcctccatggctccatggctccatggccgtggacagacggcctt 361
E E D K E A P F G S - . R G R P C L P E -

362 tggaccacatccatgtgtgtggccgtggggcaccaggtaagggtggctgtggccctgt 421

acccttgttaggacacgaccggcgaccggccgtggccactccaccaccgacacggacaca
W D H I L C W P L G A P G E V V A V P C -

422 ccggactacatttatgacttcaattcacaaaggccatgcctaccgcacgctgtgaccgcaat 481

ggcctgtatgttaataactgaagtttagtgtttccgtacggatggctgcgacactggcgtta
P D Y I Y D F N H K G H A Y R R C D R N -

482 ggcagactggagactggcctggcacaacaggacgtggccaactaacaggcgaatgtgtgtc 541

ccgtcgaccctcgaccacggaccgtgttcctgcacccggatgtcgctcacacag

FIG. 6B

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G S W E L V P G H N R T W A N Y S E C V -
aaatttctcaccaacgagactcgtgaacggagggtttgaccggccatgtttac
542 ----- 601
tttaaaggagtggttactctgagcacccatggccatccacaactggggaccggatcgactaaatg
K F L T N E T R E R E V F D R L G M I Y -
accgtggctactccgtgtccctggcgccccctcaccgttagctgtgctcatccctggcctac
602 ----- 661
tggcaccgcgtgaggcacaggacggcaggaggatggcatcgacacgaggatggaccggatg
T V G Y S V S L A S L T V A V L I L A Y -
tttaggcccgtgcaactgcacgcgcaactacatccacatgcacccatgtttccctgttcattcatg
662 ----- 721
aaatccggccgacgtgacgtgcgcgtgtatgttaggtgtacgtgtacggacaaaggaaagtac
F R R L H C T R N Y I H M H L F L S P M -
ctggcgccgtgaggcatcttcgtcaaggacgtgtgtactctggccacggttatgt
722 ----- 781
gacggcgccactcgtagaaggcagtccgtgacacgaggatggacccgggtgcgaacta
L R A V S I F V K D A V L Y S G A T L D -

FIG. 6C

782	gaggctagcgcctcacccgaggaggctgcgcgcacatcgccccaggccggccct ctccgactcgccggagtggctccttcgcgcggtagcgggtccgcggggcgccgga	841
842	E A E R L T E E L R A I A Q A P P P P - gccaccgcgtgcggctacgcggctccagggtggctgtgaccttccctttacttc cggtgccgggacggccgatgcgcccggacgtcccaaccggacactggaaatgaaag	901
902	A T A A G Y A G C R V A V T F F L Y F - ctggccaccaactactactggattctgggggtgtacacctgcacagcctcatctc gaccgggtggatgtgatgacctaagaccacccatggacgtgtggagtagaaag	961
962	L A T N Y W I L V E G L Y L H G L I F - atggccttccatcagagaagaatgtacactgtggggcttccacagtctcgctgggtctg taccggaaagaaggatctttcatggacaccccaatgtcagaagccgaccccaac	1021
1022	M A F F S E K K Y L W G F T V F G W G L - cccgctgtttcggtggctgtgtgggtcagtgatcaggactacccctggccaaacacccgggtgc gggcgacagaaggcaccgacaccccaatgtcgtggaccgggttgtggcccaacg	1081
	P A V F V A V W V S Y R A T L A N T G C - S a c	

FIG. 6D

1082 tggactttagctccggaaacaaaagtggatcatccagggtgcccattcgtggcctccatt----- 1141
accctgaactcgagggcccttgcacccatcgagggtccacgggttaggaccggaggtaa
W D L S G N K W I I Q V P I L A S I -

1142 tgctcaacttcattcattcaatatcggtccgggtgctcgccaccaaggcaggcgaa----- 1201
cacgagttgaagttaggagaagttagttatagcaggcccacaggggtgttcgtcgccctc
V L N F I L F I N I V R V L A T K Q R E -

1202 accaacggccgggtgtgacacacacggcaggcgttacccggaaagtgtcaatccacgctg----- 1261
tggttggccggccacactgtggccgtcgtcatggcccttcgacgaaatgggttagtgcgac
T N A G R C D T R Q Q Y R K L L K S T L -

1262 gtgctcatgccfcctctttggcggtccactacattgtttcatggccacaccatacaccgag----- 1321
cacgagttacggggagaaaccggcagggtgtacaaagaatgggtatgtggctc
V L M P L F G V H Y I V F M A T P Y T E -

1322 gtctcagggaacgtctggcaagtccagatgcactatgagatgctctcaactccttccag----- 1381
caggtccctgcgagaccgttcaggctcatctacgagaatgtggaaaggc
V S G T L W Q V Q M H Y E M L F N S F Q -

FIG. 6E

1382	ggatttttgtcgcaatataactgtttctgcaatggcaggttacaaggctgagaatcaag cctaaaaaacagcgtagtatatgacaaagacgttacgcgtccatgttgcactctagttc	G F F V A I I Y C F C N G E V Q A E I K -	1441
1442	aaatcttggagccgctggacactggcacttgcacttcaaggcagcggagg tttagaacctcggcgacacctgtgaccgtgacccgttgccgagcgctcgccctcg	K S W S R W T L A L I F K R K A R S G S -	1501
1502	agcagctatacgactacggcccatgggtgtcccacacaagggtgtacccaatgtcgccccgt tcgtcgatcgatcgccgggttaccacagggttacactgggttacagccggggca	S S Y S Y G P M V S H P S V T N V G P R -	1561
1562	gtgggaactcggcgtgcccccctcagccccggctactgcccactgtccaccaccaacggccac caccctgtggacggggagtcggggcggtgacgggtgacgggtgggttgcgggtg	V G L G I P L S P R L L P T A T T N G H -	1621
1622	cctcagctgcctggccatgccaaggccaggaccccgccctggagacccctcgagaccaca ggatcgacggacccgttacgggttgcgtccctgggtcgccggacacctgtgtgtgt	P Q L P G H A K P G T P A L E T L E T T -	1681

FIG. 6F

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ccacctgttatggctcccaaggacgatgggttcccaacggctcctgctcaggcctg
1682 -----
ggtgacggtaccggaccagggttcctgctaccacaaggagttgccgaggacgagtccggac
1741 -----
P P A M A P K D D G F L N G S C S G L -

gacgaggaggcctctggccctgagcgcccacctgcccctgctacaggaaggatggagaca
1742 -----
ctgctcctccggagaccggactcgccggactggacgggacgatgtccctcaccccttgt
1801 -----
D E E A S F P E R P P A L L Q E E W E T -

gtcatgtgaccaggcgctggggctggacactgatggatggacatagtgatggacatggaccca
1802 -----
cagtacactgtcccgaccccgactggacactgtatcacctacatgtctacatgt

V M

aaagatgggtgaatgtttccactcaggccctggggccaaaggaaaaaaaacagg
1862 -----
tttctaccaccaacttaagggtgagtcccgaccccggttctcccttttttttttttt
1921 -----

aa
1922 -----
tt
1981 -----

aa
1982 -----
tt
2011 -----

Enzymes that do cut:

SacI

FIG. 6G

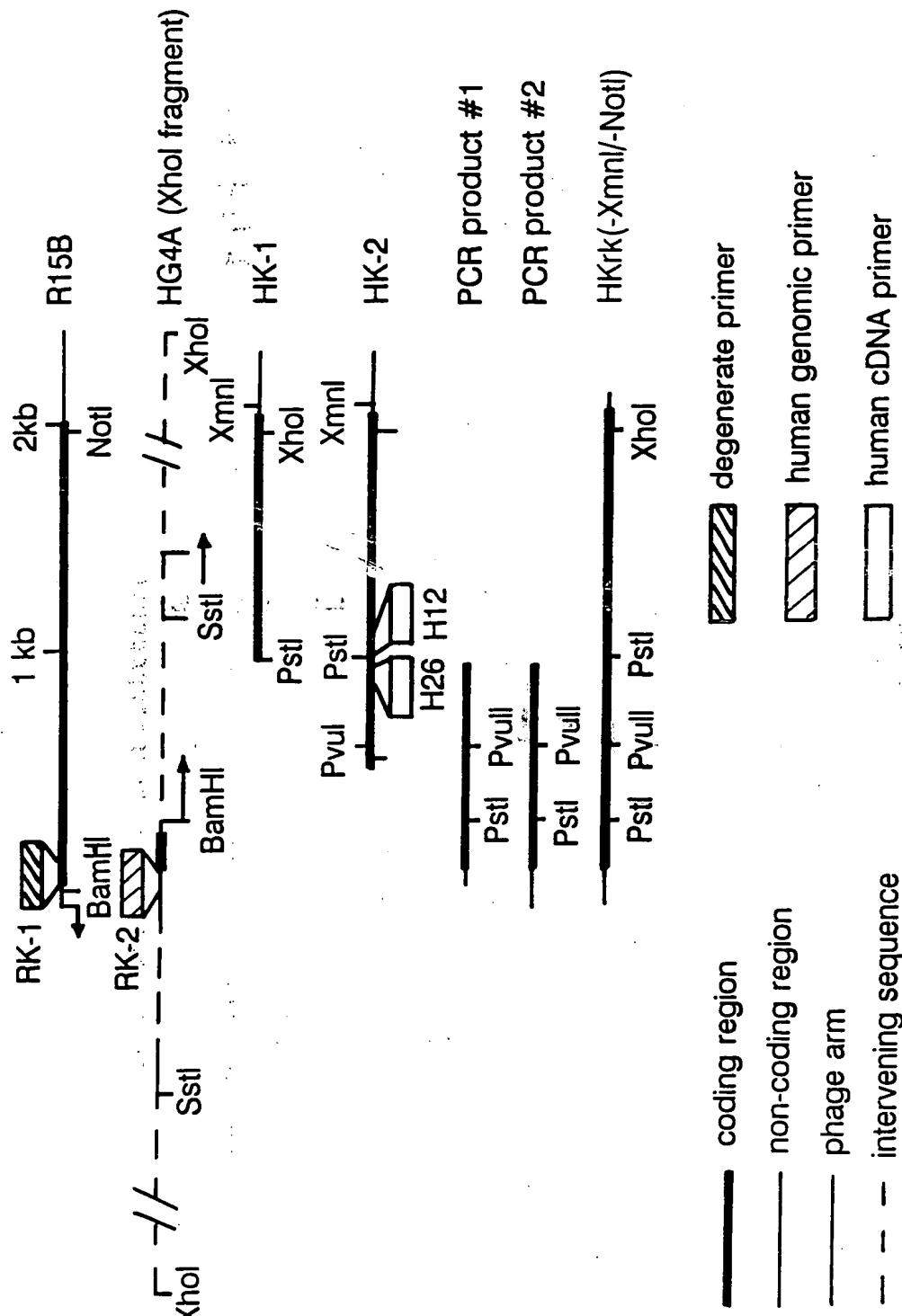


FIG. 7

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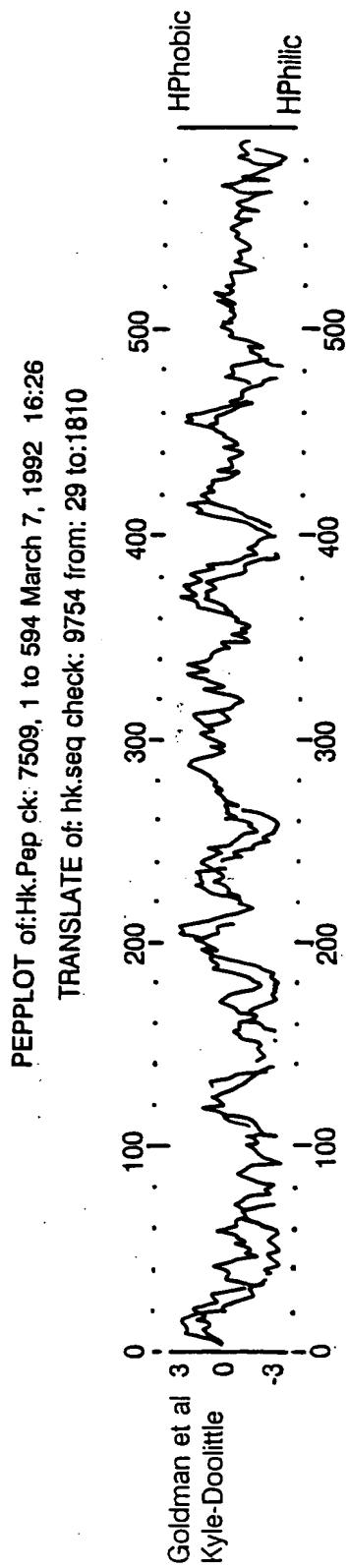


FIG. 8

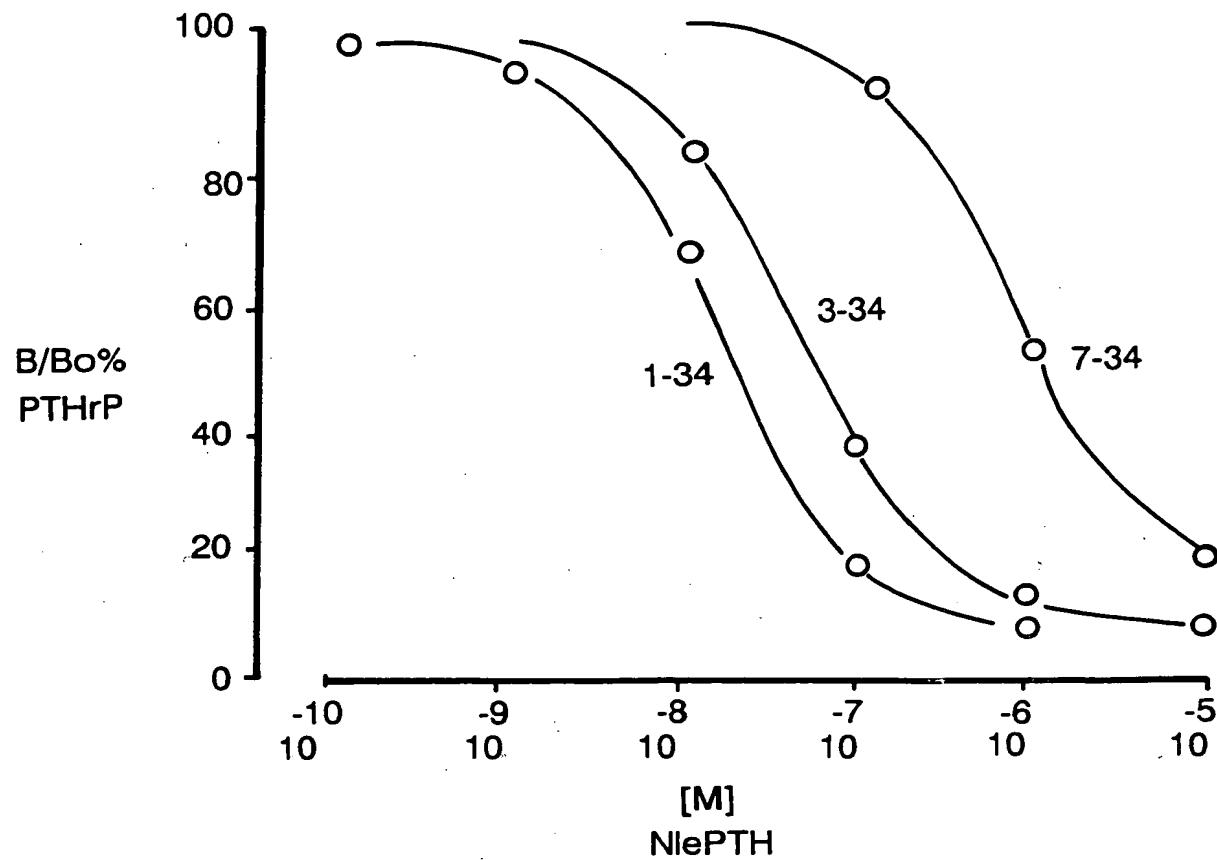


FIG. 9

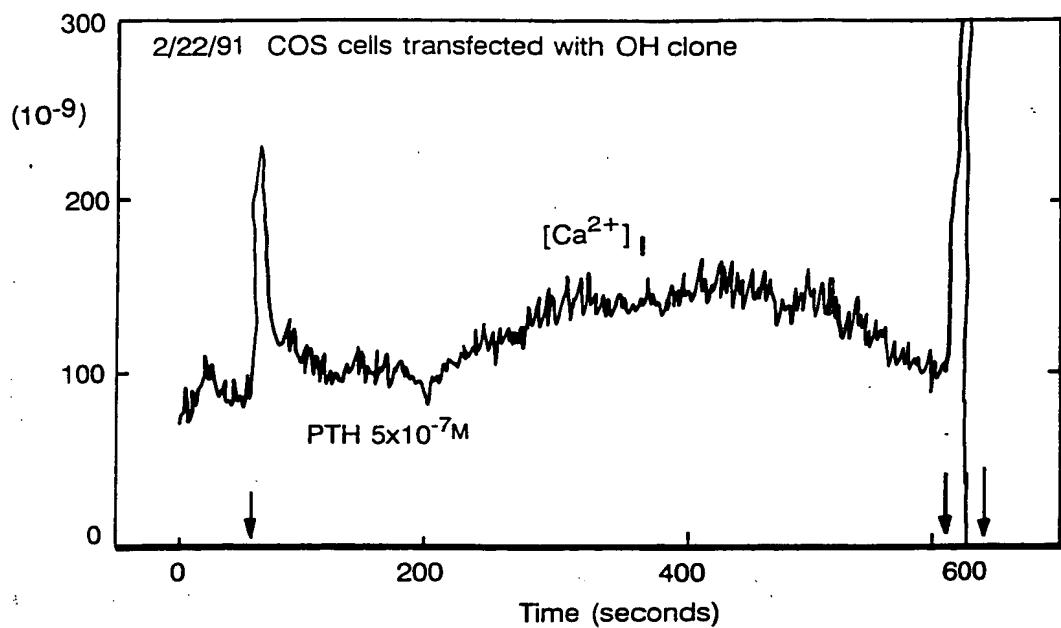


FIG. 10

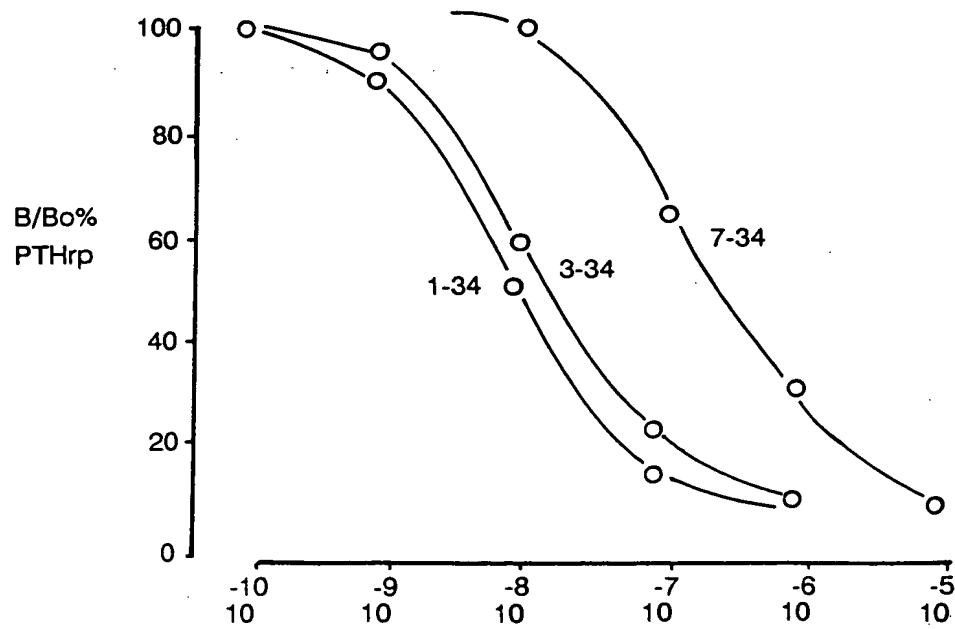


FIG. 11

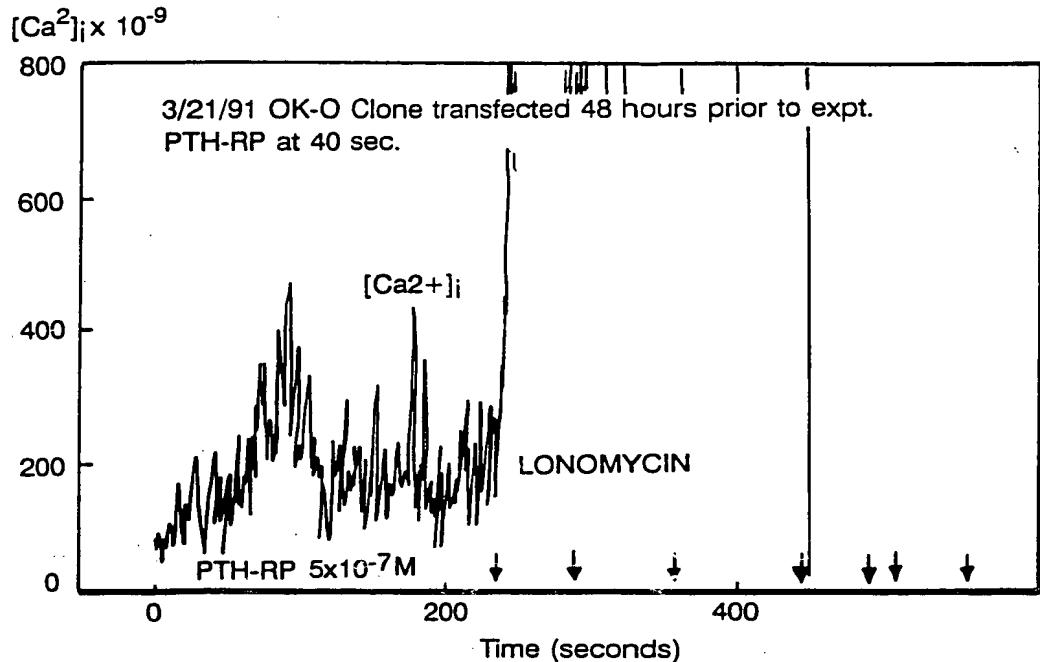


FIG. 12

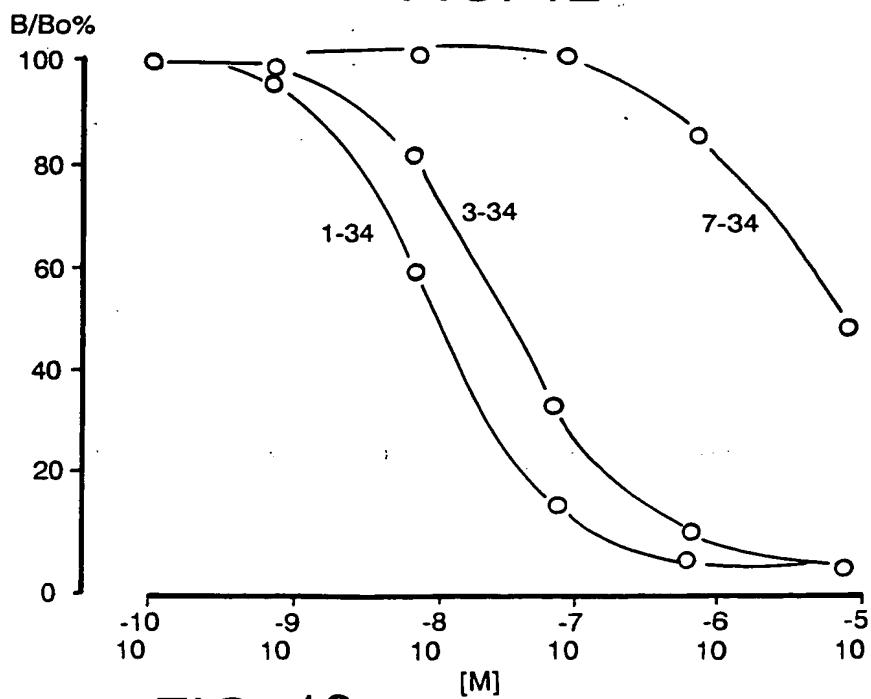


FIG. 13

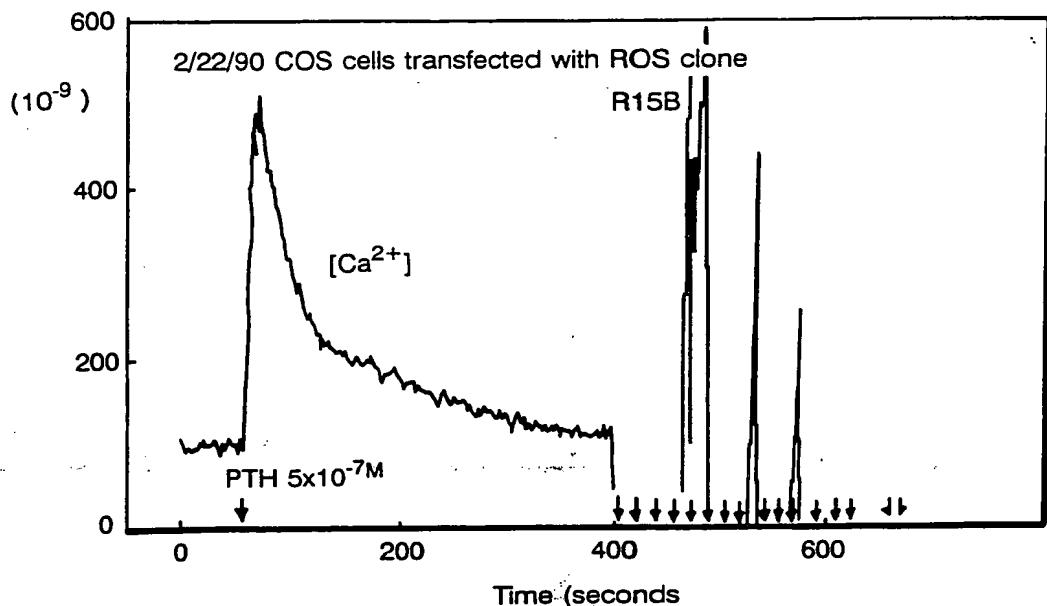


FIG. 14

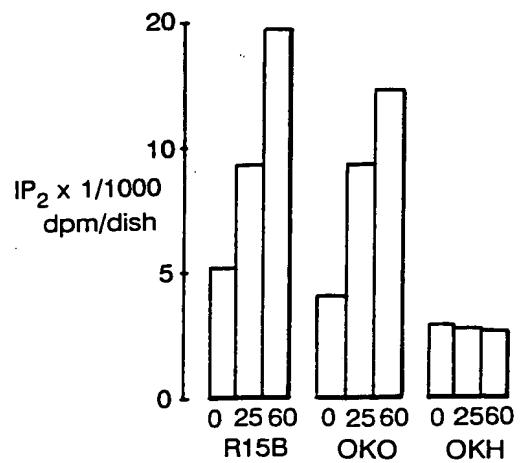


FIG. 15A

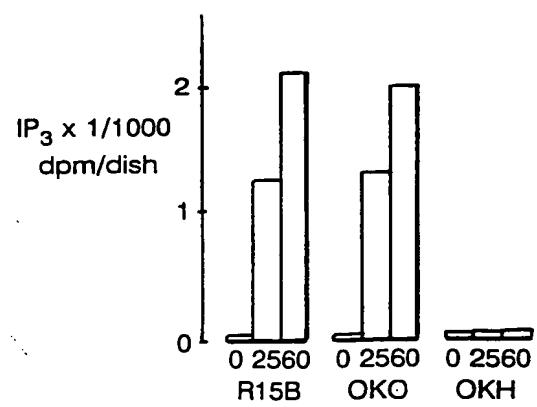


FIG. 15B

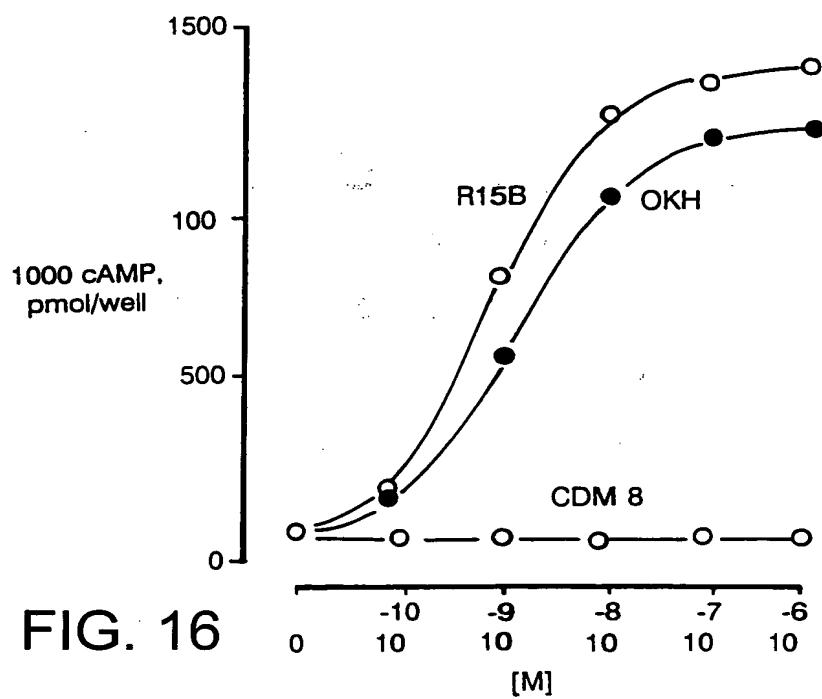


FIG. 16

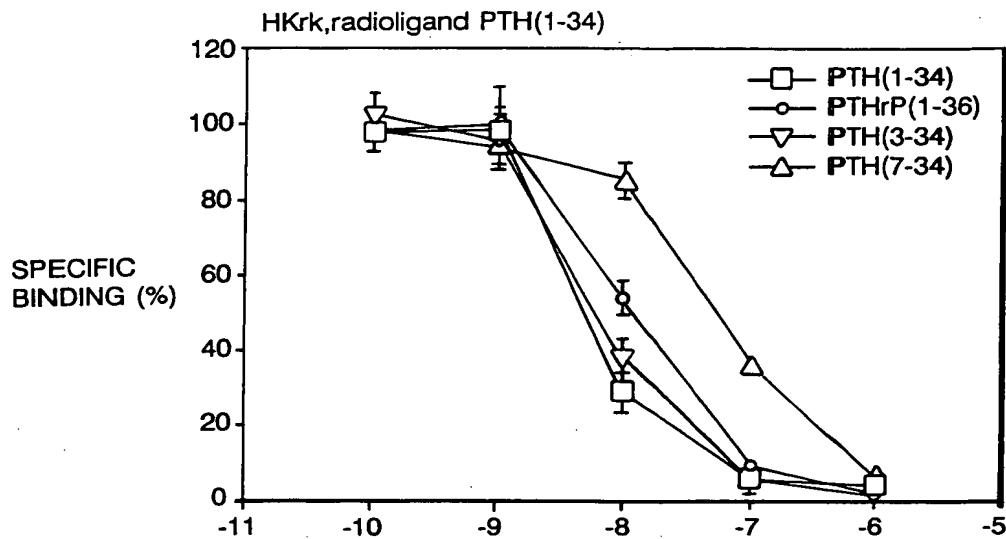


FIG. 17A

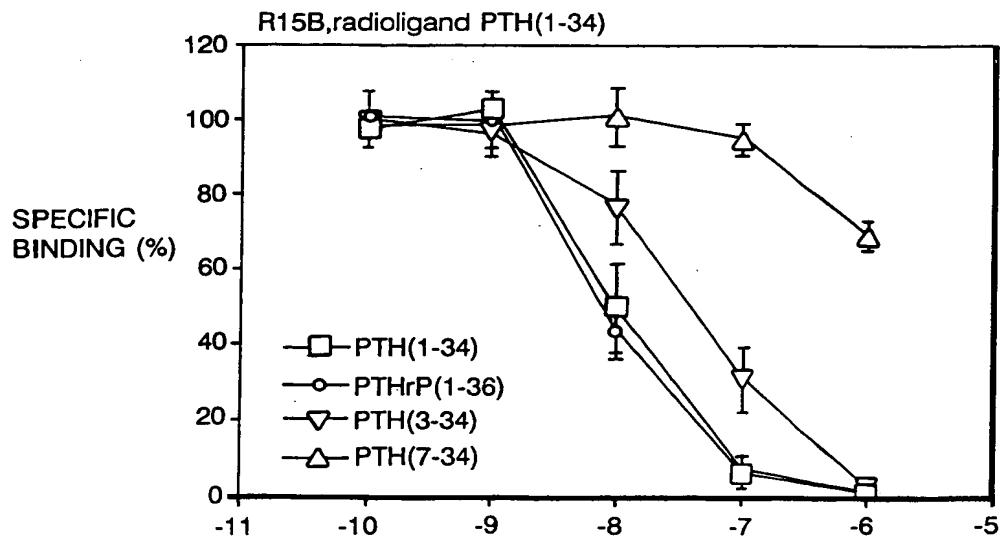


FIG. 17B

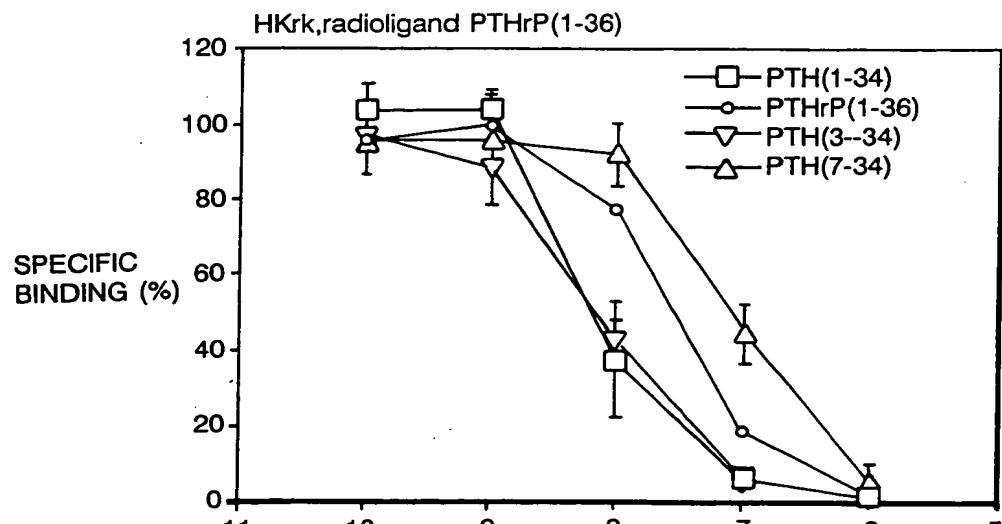


FIG. 17C

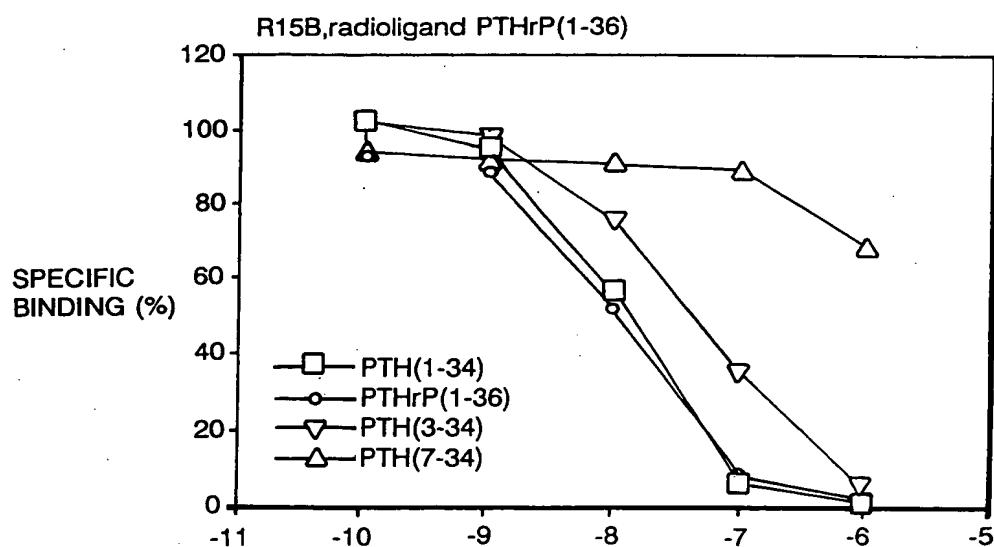


FIG. 17D

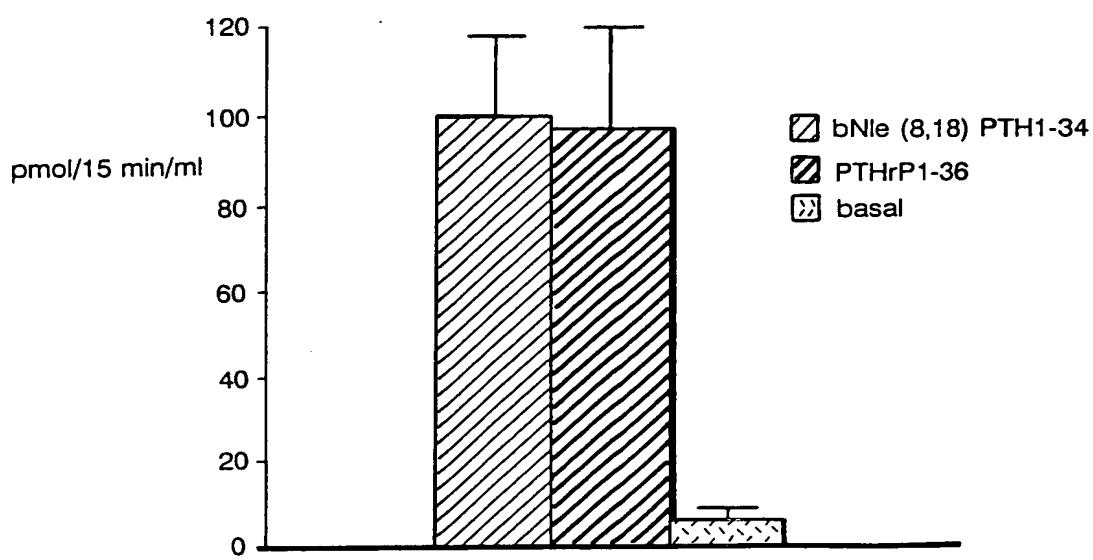


FIG. 18

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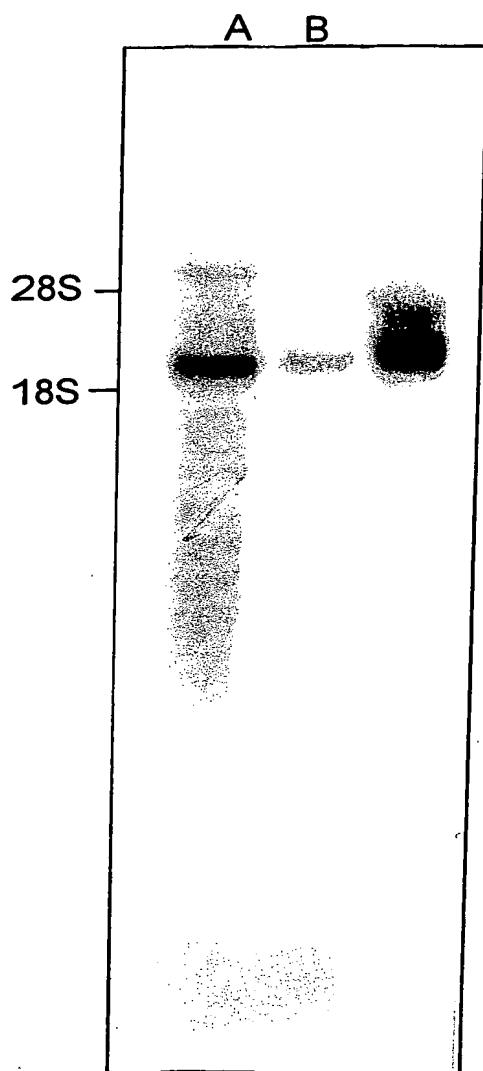


FIG. 19

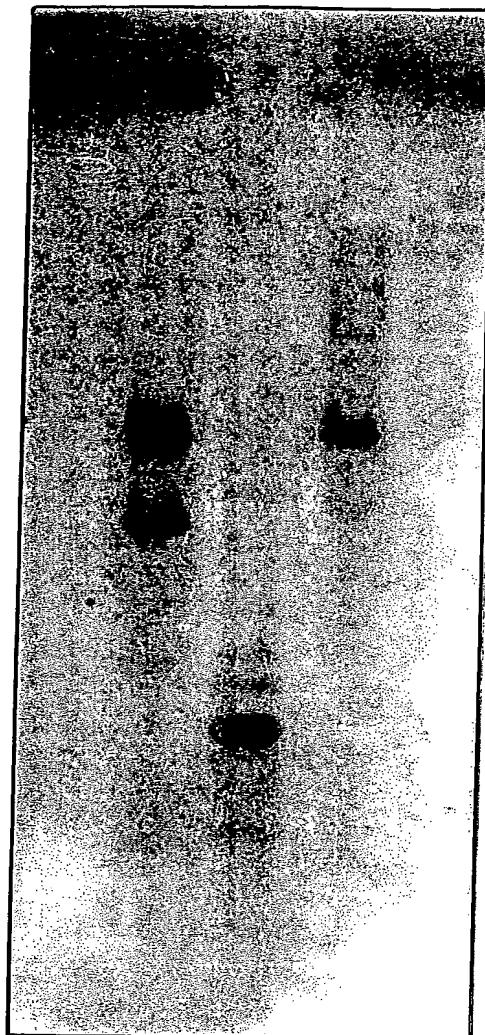


FIG. 20

RAT BONE PTH/PTH_{rP} RECEPTOR

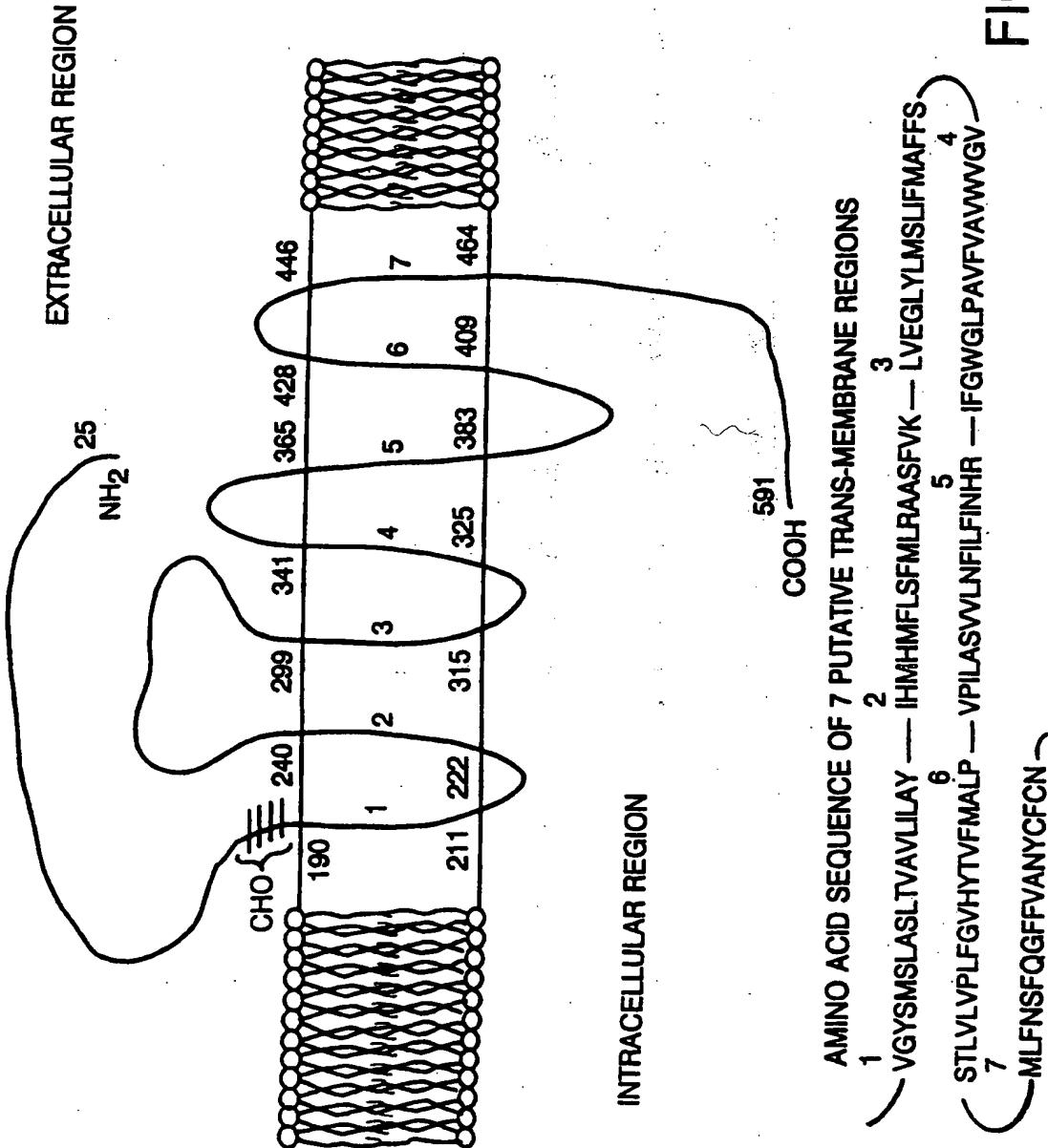


FIG. 21